

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 31, 2003, 13:28:27 ; Search time 104 seconds
(without alignments)
1305.151 Million cell updates/sec

Title: US-10-082-894-2

Perfect score: 2786

Sequence: 1 MDKYNQVQKVCVWIDWG.....LMGLPVPEMDGVPLLEQRG 526

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phase:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1900	68.2	521	5	Q8IA68
2	1900	68.2	539	5	O44742
3	1398	50.2	520	3	Q9HG4
4	1075.5	38.6	526	16	O8DCW1
5	1059	38.0	523	16	O8FCA6
6	992	35.6	505	16	O8CPY4
7	971.5	34.9	503	5	O8SR33
8	966.5	34.7	506	16	O8EW33
9	742	26.6	559	10	O9XE59
10	729	26.2	559	10	O9ZS53
11	727	26.1	560	10	O8LF55
12	715	25.7	559	10	O9SDL3
13	714.5	25.6	560	10	O94DV7
14	706	25.3	557	10	O8LD62
15	700.5	25.1	557	10	O8HI61
16	700	25.1	557	10	O94AY0

17	699	25.1	557	10	Q932F2
18	659	23.7	557	10	Q94KV1
19	639.5	23.0	516	10	Q942J3
20	626.5	22.5	550	5	Q9NG18
21	169.5	6.1	1011	16	O8EX30
22	167.5	6.0	105	3	Q9YH2
23	119	4.3	430	5	Q19519
24	115.5	4.1	545	16	O8DC63
25	110	3.9	709	5	Q21376
26	110	3.9	927	5	Q9V4N0
27	109	3.9	685	16	O8F9T4
28	109	3.9	1946	16	O8YTN2
29	108	3.9	509	11	O88548
30	107	3.8	546	16	O8EQ9
31	106	3.8	1088	10	O9SJF0
32	106	3.8	1424	10	O9FF69
33	105.5	3.8	921	10	O9XHG0
34	105	3.8	874	5	O8SR58
35	104.5	3.8	477	17	O8PTD6
36	104	3.7	715	10	O8L6C6
37	104	3.7	790	13	Q91838
38	104	3.7	1543	3	Q8X023
39	103.5	3.7	390	16	O97HE6
40	103	3.7	588	16	O8FF97
41	103	3.7	773	2	O93FB8
42	103	3.7	4840	2	O93HJ4
43	102.5	3.7	547	10	O9MA11
44	102	3.7	494	16	O8CWB5
45	102	3.7	913	4	O75061

ALIGNMENTS

RESULT 1

Q8IA68	PRELIMINARY;	PRT;	521 AA.
ID	Q8IA68;		
AC	O8IA68;		
DT	01-MAR-2003 (TREMBlrel. 23, Created)		
DT	01-MAR-2003 (TREMBlrel. 23, Last sequence update)		
DT	01-MAR-2003 (TREMBlrel. 23, Last annotation update)		
DE	Hypothetical protein F57B10.3b.		
GN	F57B10.3.		
OS	Caenorhabditis elegans.		
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;		
OC	Rhabditidae; Peloderinae; Caenorhabditis.		
OX	NCBI_TaxID=6239;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-Bristol N2;		
EX	MEDLINE=99069613; PubMed=9851916;		
RA	Waterston R.;		
RT	"Genome sequence of the nematode C. elegans: a platform for		
RT	investigating biology. The C. elegans Sequencing Consortium.;"		
RL	Science 282:2012-2018(1998).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-Bristol N2;		
RA	Greco T., Elliott G., Keppler D.;		
RT	"The sequence of C. elegans cosmid F57B10.;"		
RL	Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-Bristol N2;		
RA	Waterston R.;		
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF039713; AA012419.1; -.		
KW	Hypothetical protein.		
SQ	SEQUENCE 521 AA; 57110 MW; D13B6A484C99EC83 CRC64;		

Query Match 68.2%; Score 1900; DB 5; Length 521;
Best Local Similarity 66.7%; Pred. NO. 8.8e-148;
Matches 352; Conservative 76; Mismatches 86; Indels 14; Gaps 5;


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Db 117 IHVGVMSDGVSHIRHKAILEALEG-RNEEFVHCVSDGRDTEPRVFLKYLKVERDF 175
QY 175 IASEKYGELATIGRYAMDRDRKWERIKMAYEAI-----VGGIGQKATVDKADV---V 226
Db 176 LRTEVGKVASIAGRFYSMDRANNDTELSFRMTTGRREVGG-----DIRSHI 224
QY 227 RERYAOSSETDEFKLPKIVFSDGRVKDDDTLFFNYRADRMQICECLGLERYKDLNSSVP 286
Db 225 CAMYEGLSDTELRLPIDGRIDPKDTIIFNFRADRMQIASKFA----KNGNSMIT 280
QY 287 HPKNIQISGMTQYNKEPPFSPVTHTNVLAEWLASQGVTFQFHCATEKYPHVTFEEN 346
Db 281 -----MTEYKKDLGSKVLKICVKNKTLAEVLSSRGIRHSHIAENEKQAHVTFEEN 331
QY 347 GGREVOFQDEERCWVSPKEVATYDLKPMENNAAGVAEKVQIESGRHPLVMCNFAPDM 406
Db 332 GGREQAFSTQRTILPSP-GVQSFDAVPSASREVAMSAEIEKG-VPLVVYNLAPDM 389
QY 407 VGHGTGPEPAVKACQATDEAIGFIFEACQTYNTVLMVTSDHGNAEKMIAPDGSSEHTAHC 466
Db 390 VGHGTGNEFATKAAVEVTEDECIGKIYRACRNRRTLVITADHGNAEKMKVKGCGCKTHTT 449
QY 467 NLVPFTCSSTYFVKSTPTPTDGGKERARALRDVAPTVLQMLGLPVPPEMDG 518
Db 450 SKVPLIICERGGV-KASSSWGVDSD--HSLRDVAPTVLEIMGIPRPSMTG 498
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RESULT 8

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Q8EW33
ID Q8EW33 PRELIMINARY; PRT; 506 AA.
AC Q8EW33;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Phosphoglycerate mutase.
GN MYPE3740.
OS Mycoplasma penetrans.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=28227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HF-2;
RX MEDLINE=22354719; PubMed=12466555;
RA Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K.,
RA Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;
RT "the complete genomic sequence of Mycoplasma penetrans, an
RT intracellular bacterial pathogen in humans.";
RL Nucleic Acids Res. 30:5293-5300(2002).
DR EMBL; AP004171; BAC44163.1; -.
KW Complete proteome.
SQ SEQUENCE 506 AA; 56436 MW; 915210E83497B289 CRC64;
```

Query Match 34.7%; Score 966.5; DB 16; Length 506;
Best Local Similarity 41.2%; Pred. No. 6.5e-71;
Matches 216; Conservative 93; Mismatches 178; Indels 37; Gaps 13;

```
QY 11 VCLVVDGWSLSDQHGNAIAKAKTPTMDKL-----CSGNWQKLEAHGLHVLGPELGM 64
Db 10 VLLAVLDGYSFKDQTKGNALNNAKTPTMDNLVKEYDHC-----YIEASGEYVGLPDQIG 64
QY 65 NSEVGHNLNIGAGRIYQDIVRINLAVORNEFTVNPQIVASAEKAKGSGRLHLGLVSDG 124
Db 65 NSEVGHNLNIGAGRIYVGLSLNQDIKTKKFDNSKNTLLEAINAKKNSNIHMLGSLSPG 124
QY 125 GVSHIDHLFALITRAFQKQVVKVFIHFADGDRDTSPTSGAGYLEQLLOFIASEKY-GEL 183
Db 125 GVHSEHQHIFEMIRIVSENGL-KPVIHVFGDGRDVAQPSIISSLRLNDVL--KKYFGTI 181
QY 184 ATITGRYAMDRKWRERIKMAYEIVGGIGQKATVDKADVVRERYAQSETDFELKPIV 243
Db 182 ATISGRFYSMDRKRWERTKQAVDNLG--ISNNYFQNPIDYVKNQYSENFDFELVLPAR 239
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QY 244 FSDGRV-KDDDTLFFNYRADRMQICECL-GLERYKDLNSSVPHP-KNIQISGMTQYN 300
Db 240 INSNNVVKDNDAVIHANFRDRAQISHLFCGSTVVEEKND---HPLKNLYIATMMTYE 296
QY 301 KEPPFSPVTHTNVLAEWLASQGVTFQFHCATEKYPHVTFEENFGREVGQFQDEBRCM 360
Db 297 GITPTSLFPTVVVKNFTGFEVANSGLTQLRIATEKYAHVTFEFGDGVVDLKNESKIL 356
QY 361 VPSPEKAVATYDLKPMENNAAGVAEKVQIESGRHPLVMCNFAPDMVGHGTGKEPEPAYKAC 420
Db 357 VDS-KKVTGYDEVPAMSAVEITDKLIENID--KPDVIVLNFANADMVGHGTGKYNELAI 413
QY 421 QATDEAIGKIFEACQTYNTVLMVTSDHGNAEKMIAPDGSSEHTAHCNLVPTCSSTKTFE 480
Db 414 EALDSQLARDIQKIKELNGTMTFADHGNAEVMLDDNNPVTKHTTNPVIFISNNKDKVF 473
QY 481 KSTPTGDDGKERARALRDVAPTVLQMLGLPVPPEMDGVPLLEQ 524
Db 474 -----NKPGLSGNVAPTILDFMGLFIAPADMKKSLLK 506
```

RESULT 9

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Q9XE59
ID Q9XE59 PRELIMINARY; PRT; 559 AA.
AC Q9XE59;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Phosphoglycerate mutase (EC 5.4.2.1).
GN PGAM.
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; famids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Desire;
RA Westram A., Kossmann J.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF047842; AAD24857.1; -.
DR InterPro; IPR006124; Metalloenzyme.
DR InterPro; IPR005995; Pgm_bpd_ind.
DR Pfam; PF01676; Metalloenzyme; 1.
DR ProDom; PD004429; Pgm_bpd_ind; 1.
DR TIGRFAMs; TIGR01307; pgm_bpd_ind; 1.
KW Isomerase.
SQ SEQUENCE 559 AA; 61257 MW; 68CBEB23585262E0 CRC64;
```

Query Match 26.6%; Score 742; DB 10; Length 559;
Best Local Similarity 34.2%; Pred. No. 2.3e-52;
Matches 186; Conservative 92; Mismatches 214; Indels 52; Gaps 16;

```
QY 11 VCLVVDGWSLSDQHGNAIAKAKTPTMDKLCSG---NWQKLEAHGLHVLG-LP-BGLMGNS 66
Db 22 VAVILVDGWEAKPNEYNALSAETPVMSLSKGAPEHRLIKAHGNVAGLPTDEDDMGNS 81
QY 67 EVGHNLNIGAGRIYQDIVRINLAVORNEFTVNPQIVASAEKAKGSGRLHLGLVSDGV 126
Db 82 EVGHNLNIGAGRIYQAGAKLVDLALASKGIYDGEQKIVYQECFEKGT--LHLIGLVSDGV 139
QY 127 HSHIDHLFALITRAFQKQVVKVFIHFADGDRDTSPTSGAGYLEQLLOFIASEKY---GE 182
Db 140 HSRIDQLLLKGAERGAERKIRVHALTDGRDLGDSVGVGMETLENDLAKLRQGGVDAR 199
QY 183 LATITGR-YVAMDR-DKRWRERIKMAYEIVGGIGQKATVDKADVVRERYAQSETDFELK 240
Db 200 VASGGRMYTMDRVENDWDVVKGWDQAQVLGEPHFKDPVEAIKKLRQEPNTSDQYLA 259
QY 241 PIVESDD-----GRVKDDDTLFFNYRADRMQICECLGLERYKDLNSSVPHPKNIQIS 295
Db 260 PFVIVDDNGKVPGLDGDVAVTFNFRADRMVLALEYEDF-DKDFRVRVPK-IHVAG 317
```

QY 296 MTQYNKEFFPPSLF-----PPVTHTNVLAELASQGVTOFHCAETEKYPHVTFEFGNGREV 351
 Db 318 MLQYDGLKLPNKLVSPEIDRTS--GEYLVNGVTFACSETVAFGHVTFWNGNRSG 375
 QY 352 QFOD--EERCWVSPKEVATYDLKPEMNAAGVAEKVQIESGRHPLVMCNFAPPDMVGH 409
 Db 376 YFEKLEEEVEIPSDSGI--TENVKPKMALEAETRDAILSHKFDQVRNIPNSDMVGH 434
 QY 410 TGFEPVAVACATDEAIGKIFECACOTYNNVLMVTSDHGNAEKMIAPDGSSEH-----461
 Db 435 TGDIKATIEACRAADGVKMLIEIQVGGIFLVTADHGNADWVRNKKGEPLLDKNGN 494
 QY 462 ----TAHTCNLVPTCSSKTFV-----FKSTPTPTGDDGKERARALRDVAPTQLQMLPLVP 513
 Db 495 IQILTSHTELPVPIAGGPGCLLPVGRFRTDLPFG-----GLANVAATFNNLHGFEP 546
 QY 514 PEMD 517
 Db 547 SDYE 550

RESULT 10

Q92553 PRELIMINARY; PRT; 559 AA.
 ID Q92553
 AC Q92553
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Apqm protein (FC 5.4.2.1).
 GN APQM.
 OS Malus domestica (Apple) (Malus sylvestris).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Rosales; Rosaceae; Maloideae; Malus.
 OX NCBI_TaxID=3750;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Golden Delicious; TISSUE=Pericarp;
 RA Krebitz M., Ferreira F., Scheiner O., Breiteneder H.;
 RT "Phosphoglyceromutase from apple."
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ004915; CA006215.1; -
 DR InterPro; IPR006124; Metalloenzyme.
 DR InterPro; IPR005995; Pgm_bpd_ind.
 DR Pfam; PF01676; Metalloenzyme; 1.
 DR ProDom; PD004429; Pgm_bpd_ind; 1.
 DR TIGRFAMs; TIGR01307; Pgm_bpd_ind; 1.
 KW Isomerase.
 SQ SEQUENCE 559 AA; 60794 MW; F97E500F54B03CCD CRC64;

Query Match 26.2%; Score 729; DB 10; Length 559;
 Best Local Similarity 34.5%; Pred. No. 2.8e-51;
 Matches 193; Conservative 84; Mismatches 196; Indels 86; Gaps 22;

QY 13 LVVIDGWSLSDQHGNNAIAKAKTPIIMDKLCSG---NWOKLEAGLHVGLP-EGLMGNSV 68
 Db 24 LIVLDGWEANADQYNCIHVAETPVMSLKGAPERWRLVRAHGTAVGLPTEDDGMNSV 83
 QY 69 GHLNTGAGRVYQDIVRINLAVQ-----RNEFTNPNQIVASAEAKKSGSL 115
 Db 84 GHNALGAGRIFAGAKLVDAALASGKIFEGEGFKVYKESFETN-----TL 128
 QY 116 HLGLVSDGVSHTDHLFALIRAFKQLQVQKVFIFHFDAGDRDTSPTSGAGYLEQLQPI 175
 Db 129 HLIGLSDGVSHTDHLQALLLLKLGASEQAKIRVHILTDGRLDGGSSVGAELIENDL 188
 QY 176 AS-EK-YGELATTGR-YAMDR-DKWERIKWAYE-IVGGIGQKATVDKVDVRE 228
 Db 189 AKLREKGVDAQIASGGGRVYTMTRYENDWSVVKRGWDAQVLGEAPYK--FKNAVEAIKT 246
 QY 229 RYAQ-SETDEFKLPVFSDD-----GRVKDDDTLFFNVRADMRQICECLGLERYKDLN 282
 Db 247 LRAEPNANDQYLPFPVIVDDSGKPVGPVVDGDAVVTFNFRADRMVMIKAL----ETADF 303

QY 283 --SSVPHPKNIOISGMTQYNKEFFPPSLF-----PPVTHTNVLAELASQGVTOFHCAETE 336
 Db 304 KFDVRVPAK-IRYAGMLQYDGLKLPVPEIDRTS--GEYLVYNGVTFACSETV 360
 QY 337 KYPHVTFEFGNGREVQFOD--EERCWVSPKEVATYDLKPEMNAAGVAEKVQIESGRH 394
 Db 361 KFGHVTFFWNGNRSGYFNDKMEYVEIPSDSGI--TENVQPKMAVEIAEKARDAILSGKF 419
 QY 395 PLVMCNFAPPDMVGHGTGKEFPAVKACQATDEAIGKIFECACOTYNNVLMVTSDHGNAEKMI 454
 Db 420 EQVRVNLPGMDVGHGTGDIETATVACAADEAVKIILDAIEKVGVIYVVTADHGNADMV 479
 QY 455 APDGSSEH-----TAHTCNLVPTCSSKTFV-----PKSTPTPTGDDGKERARALR 498
 Db 480 KRNTGQPLDKSGNLIQILTSHTLQVPVPIAIGGPGLAGVGRFRKDLPSG-----GLA 531
 QY 499 DVAPTQLQMLPLVPPEMD 517
 Db 532 NVAATVMNLHGFAQPSDYE 550

RESULT 11

Q8LF55 PRELIMINARY; PRT; 560 AA.
 ID Q8LF55
 AC Q8LF55
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Putative 2,3-bisphosphoglycerate-independent phosphoglycerate mutase.
 DE Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N.,
 RA Felmann K.A., Flavell R.B., White O., Salzberg S.L.;
 RT "Full-length messenger RNA sequences greatly improve genome annotation."
 RL Genome Biol. 0:0-0(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
 RA Felmann K.;
 RT "Full-length cDNA from Arabidopsis thaliana."
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY085044; AAM61601.1; -
 DR InterPro; IPR006124; Metalloenzyme.
 DR InterPro; IPR005995; Pgm_bpd_ind.
 DR Pfam; PF01676; Metalloenzyme; 1.
 DR ProDom; PD004429; Pgm_bpd_ind; 1.
 DR TIGRFAMs; TIGR01307; Pgm_bpd_ind; 1.
 SQ SEQUENCE 560 AA; 60699 MW; C251A9BFF6FA07A CRC64;

Query Match 26.1%; Score 727; DB 10; Length 560;
 Best Local Similarity 35.0%; Pred. No. 4e-51;
 Matches 192; Conservative 86; Mismatches 205; Indels 66; Gaps 20;

QY 13 LVVIDGWSLSDQHGNNAIAKAKTPIIMDKLCSG---NWOKLEAGLHVGLP-EGLMGNSV 68
 Db 25 LIVLDGWESEDPPQYNCIHKAPTAPMDSLKDGKPDTRLIKAHGTAVGLPSDDDMGNSV 84
 QY 69 GHLNTGAGRVYQDIVRINLAVORNEFTNPNQIVASAEAKKSGRLHLGLVSDGVSHT 128
 Db 85 GHNALGAGRIFAQAKLVDAALASGKIYDEDEGFKYISFEKGT--VHLIGLSDGVSHT 142
 QY 129 HTDHLFALIRAFKQLQVQKVFIFHFDAGDRDTSPTSGAGYLEQLQFIASEKY----GELA 184
 Db 143 RLDDQVLLKLGFAERKAKRIRVHILTDGRLDGGSSVGVFETLEADLAALRSKGVDAQVA 202


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QY 127 HSHIDHLFALIRAFKQLQVPKVIHFHFDAGDRDTSPTSGAGYLEQLLOFTASEK-----YGE 182
D 140 HSLRDQVQLLKASERGAIRIRVHILTDGRVDLDCSSGVFVETLESLSQLRDKGIDAR 199
QY 183 LATITGR-YYAMDR-DKRWERIKMAYEA-IVGGIGOKATVDKAVDVVRERYAQSE-TDEF 238
D 200 IASGGGRMYTMDRYENDMDVVKRGWDAQVILGEAPYK--FQNAVEAVTLRAETKASDQY 257
QY 239 LKPIVFSDD-----GRVKDDDTLIFNRYRADRMQICEGLGLERYKDLN--SSVPHPKNI 291
D 258 LPFVIVDESCKSVGPVVDGDAVVTNFNFRADRMVLAALAKL---EYADFDFKFDVRYVPK-I 313
QY 292 QISGMTQYNKKEFPFSLF-----PPVTHTNVLAELASQGVTOFPCA-EETEKYPHVTFFFN 346
D 314 RVAGMLQYDGLKLPKSHYLVSPPEIERTS--GEYLVKNGVTRFACRHETVTKFHVTFWFN 371
QY 347 GGEVFOFODEERCMPSPKEVA--TYDLKPEMNAAGVAEKVQIESGRHPLVMCNFAPPD 405
D 372 GNRSGYFDETKEEYVEIPSDIGITFNVKPKMKALEIAERADAILSGKFDQVRVNLPGND 431
QY 406 MVGHTGKFFPAVKACQATDEAIGKIFACQTYNVLMVTSDHGNAEKMIAPDQSEH---- 461
D 432 MVGHTGDIATVVACKAADAENKIIILDAIEQVGGIYLVTDHGNADMDVKNKSGQPLD 491
QY 462 -----TAHCTNLVPTCSKTF-----VFKS-----TPPTGDDGKERARALRDVAPT 506
D 492 KNGGIQILTSHTLQVPVPAIGGPGHGPVKFRSDIQT-----GLANVAATVMN 540
QY 507 LMGLPVPPEMD 517
D 541 FHGFEAPADYE 551

RESULT 14
Q8LD62
ID Q8LD62 PRELIMINARY; PRT; 557 AA.
AC Q8LD62;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Putative 2,3-bisphosphoglycerate-independent phosphoglycerate
DE mutase.
GN AT1G09780.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
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RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
RA Quach H.L., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.C.,
RA Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
RA Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Arabidopsis Full Length cDNA Clones.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY086182; AAM64261.1; -
DR EMBL: AY150432; AAN12974.1; -
DR EMBL: BF000773; AAN31912.1; -
DR InterPro: IPR006124; Metalloenzyme.
DR InterPro: IPR005995; Pgm_bpd_ind.
DR Pfam: PF01676; Metalloenzyme; 1.
DR ProDom: PD004429; Pgm_bpd_ind; 1.
DR TIGRfams: TIGR01307; Pgm_bpd_ind; 1.
SQ SEQUENCE 557 AA; 60579 MW; D5FC3D06A963B9AB CRC64;

Query Match 25.3%; Score 706; DB 10; Length 557;
Best Local Similarity 34.4%; Pred. No. 2.2e-49;
Matches 189; Conservative 85; Mismatches 213; Indels 62; Gaps 21;

QY 11 VCLVVDGWLSDSQHGNIAIAKAKTPIMDKLCG---NMQKLEAHGLHVLGP-EGLMGNS 66
D 21 IAVIVLDGGESAPQYNCIHNAPTPAMDSLKHGAPDTWTLKAHGTAVGLPSEDDMGNS 80
QY 67 EYGLNIGAGRIYQDIVRINLAVORNEVTNPQIVASAEARAKKSGRLHLGLVSDGGV 126
D 81 EVGHNALGAGRIFAQAGKALCQALASGKIFEGEGFYVSESE--TNTLHLVGLLSDGGV 138
QY 127 HSHIDHLFALIRAFKQLQVPKVIHFHFDAGDRDTSPTSGAGYLEQL-LQFIASEKYG---E 182
D 139 HSLRDQVQLLKASERGAIRIRVHILTDGRVDLDCSSGVFVETLESLSQLRDKGIDAR 198
QY 183 LATITGR-YYAMDR-DKRWERIKMAYEA-IVGGIGOKATVDKAVDVVRE-RYAAQSETDEF 238
D 199 IASGGGRMYTMDRYENDMDVVKRGWDAQVILGEAPYK--FKNAVEAVTLRAETKASDQY 256
QY 239 LKPIVFSDD-----GRVKDDDTLIFNRYRADRMQICEGLGLERYKDLNSSVPHPKNIQI 293
D 257 LPFVIVDESCKSVGPVVDGDAVVTNFNFRADRMVLAALAKL---EYADFDFKFDVRYVPK-I 314
QY 294 SCMTQYNKKEFPFSLF-----PPVTHTNVLAELASQGVTOFPCA-EETEKYPHVTFFFN 349
D 315 AGMLQYDGLKLPKSHYLVSPPEIERTS--GEYLVKNGVTRFACRHETVTKFHVTFWFN 372
QY 350 EYQFOD--EERCMPSPKEVATYDLKPEMNAAGVAEKVQIESGRHPLVMCNFAPPD 407
D 373 SGYFNEKLEEYVEIFSDSGI-SFNVPKMALEIGEKAARDAILSGKFDQVRVNLPGND 431
QY 408 GHTGFEPVAVKACQATDEAIGKIFACQTYNVLMVTSDHGNAEKMIAPDQSEH----- 461
D 432 GHTGDIATVVACKAADAENKIIILDAIEQVGGIYLVTDHGNADMDVKNKSGQPLD 491
QY 462 -----TAHCTNLVPTCSKTFV-----FK-----STPPTGDDGKERARALRDVAPT 508
D 492 GRLQILTSHTLQVPVPAIGGPGHGPVKFRSDIQT-----GLANVAATVMN 540
QY 509 GLPVPPEMD 517
D 541 GFVAFSDYE 549

RESULT 15
Q8H161
ID Q8H161 PRELIMINARY; PRT; 557 AA.
AC Q8H161;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Putative 2,3-bisphosphoglycerate-independent phosphoglycerate
DE mutase.

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